

## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

### Listing Of Claims

1. (Currently amended) A composition comprising a protein in crystalline form wherein the protein ~~has at least 90% identity with residues 605-883 of SEQ. ID No. 1.~~ consists of SEQ ID NO: 3.
2. (Currently amended) A composition according to claim 1 wherein the protein ~~has at least 95% identity with residues 605-883 of SEQ. ID No. 1.~~ is present in the protein crystal as a dimer.
3. (Cancelled)
4. (Currently amended) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution having a value less greater than 3.0 Angstroms.
5. (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice in a P<sub>3</sub>21 space group.
6. (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=72.12Å, b= 72.12Å and c=241.62Å.
7. (Cancelled)
8. (Cancelled)
9. (Currently amended) A method ~~for forming a crystal of a protein~~ comprising:

forming a crystallization volume comprising[[:]] a precipitant solution and a protein wherein the protein has ~~at least 90% identity with residues 605-883 of SEQ. ID No. 1; and that~~ consists of SEQ ID NO: 3; and

~~storing the crystallization volume under conditions suitable for crystal formation of the protein.~~

forming a crystalline form of the protein in the crystallization volume.

10. (Currently amended) A method according to claim 9 wherein the protein ~~has at least 95% identity with residues 605-883 of SEQ. ID No. 1.~~ is present in the protein crystal as a dimer.

11. (Cancelled)

12. (Currently amended) A method according to claim 9 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution having a value less greater than 3.0 Angstroms.

13. (Original) A method according to claim 9 wherein the protein crystal has a crystal lattice in a P<sub>3</sub>2<sub>1</sub> space group.

14. (Original) A method according to claim 9 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=72.12Å, b= 72.12Å and c=241.62Å.

15. (Currently amended) A method according to claim 9, the method further comprising:  
diffracting the protein crystal to produce a diffraction pattern; and  
solving the structure of the protein from the diffraction pattern.

16. (Cancelled)

17. (Currently amended) A composition comprising ~~an isolated~~ a protein consisting of ~~SEQ. ID No. 3.~~ SEQ ID NO: 3.

18-25. (Cancelled)

26. (New) A method according to claim 15, the method further comprising:  
performing rational drug design using the solved structure; and  
identifying an entity that associates with the protein.
27. (New) A method according to claim 26 wherein the protein is present in the protein crystal as a dimer.
28. (New) A method according to claim 26 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=72.12\text{\AA}$ ,  $b=72.12\text{\AA}$  and  $c=241.62\text{\AA}$ .
29. (New) A method according to claim 26 wherein the protein crystal has a crystal lattice in a  $P3_221$  space group.
30. (New) A method according to claim 26, the method further comprising:  
selecting one or more entities based on the rational drug design; and  
contacting the selected entities with the protein.
31. (New) A method according to claim 26, the method further comprising measuring an activity of the protein when contacted with the one or more entities.
32. (New) A method according to claim 26, the method further comprising:  
comparing activity of the protein in a presence of and in the absence of the one or more entities; and  
selecting entities where activity of the protein changes depending whether a particular entity is present.
33. (New) A method according to claim 26, the method further comprising:  
contacting cells expressing the protein with the one or more entities; and  
detecting a change in a phenotype of the cells when a particular entity is present.